

## REPLACEMENT SHEET

><MW: 120922

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RSFSGLTYLKSLYLDGNQLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLG  
QNCYYRNPCYVSYSIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTLEYLYNNMIAKI  
QEDDFNNLNQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSN  
SLQHVPPRWFKNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASM  
NLSQAFSSLKSLKILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQF  
KRLKVIDLSVNKISPSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNK  
EASFMSVNESCYKYGQTLDSLKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQP  
LAELRYLDFSNNRLDLLHSTAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLOK  
LMMNDNDISSSTSRTESESLRTEFRGNHLDVLRREGDNRYLQLFKNLLKLEELDLSKN  
SLSFLPSGVFDGMPPNLKNLSLAKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSN  
CSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLL  
HHNRFLCTCDVWFVWWVNHTVETIPYLATDVTCVGPAGAHKGQSVISLDLYTCELDLTNL  
ILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQRLISPCCYDAFIVYDTK  
DPAVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQSIQLSKKTVFVMTDK  
YAKTENFKIAFYLSHQRLMDEKVDVILIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQ  
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FIG. 1

# REPLACEMENT SHEET

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GAACAATTACATTATTTTTCAGATATGATAAGTATGCAAGGAGTTGCAGATTCAAAAAACAAA
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AGTAAAAAATAGTATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTTTCTTCTCCTCAAA

```

FIG. 2A

# REPLACEMENT SHEET

TGCCTGAATCTGTGAGGAAATCTCATTAGCCAAACTCTTAATGGCAGTGAATTCCAACCT  
 TTAGCAGAGCTGAGATATTGGACTTCTCCAACAACCGGCTTGATTACTCCATTCAACA  
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 CTGATGATGAACGACAAATGACATCTCTTCCACCAGCAGGACCATGGAGAGTGAGTCT  
 CTTAGAACTCTGGAATTGAGAGGAAATCACTTAGATGTTTATGGAGAGAAGGTGATAAC  
 AGATACTTACAATTATTCAAGAACTGCTAAATTTAGAGGAATTAGACATCTCTAAAAAT  
 TCCCTAAGTTTCTTGCCCTCTGGAGTTTGTATGGTATGCCCTCCAAATCTAAAGAATCTC  
 TCTTTGGCCAAAAATGGGCTCAAAATCTTTCAGTTGGAAGAAAATCCAGTGTCTAAAGAAC  
 CTGGAATCTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAAC  
 TGTTCAGAAAGCCTCAAGAAATCTGATCTTAAAGAAATAAATAAATCAGGAGTCTGACGAAG  
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 ATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTCAACAATCTGAAGATGTTGCTTTTG  
 CATATAATCGGTTTCTGTGCACTGTGATGCTGTGGTTTGTCTGGTGGTTAACCAT  
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 AAGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG  
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 CACCTCTATTTCTGGGATGTGGTATATTTACCATTCTGTAAAGGCCAAGATAAAGGGG  
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 GCTCACCCATATCTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAAATCATGTGGCC  
 TATAGTCAGGTGTTCAAGGAAACGGTCTAGCCCTTCTTTTGCAAAACACAACTGCCTAGTT  
 TACCAAGGAGAGGCTGTC

FIG. 2B

## REPLACEMENT SHEET

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQNDSVIAECSNRRLQEVPT  
VGKYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGA  
FLNLKNLRELLLEDNQLPQIPSGLPESLTELSTIQNNIYNITKEGISRLINLKNLYLAWN  
CYFNKVCEKTNIEDGVFETLTNLELLSLSFNLSHVPPKLPSSLRKLFLSNTQIKYISEE  
DFKGLINLTLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTLRLYNLSSTSLR  
KINAAWFKNMPHLKVLDLEFNVLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINIS  
RNFSKLLSLRALHLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSL  
EIIYLSNRISPLVKDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTREPLIKPQCA  
AYGKALDLSLNSIFFIGPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNN  
RLDFDNASALTELSDEVLDSLNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLT  
DKYNLESKSLVELVFSGNRLDILWDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFL  
NLPASLTEHINDNMLKFFNWTLLOQFPRELLDLRGNKLLFLTDSLSDFTSSLRTLLLS  
HNRISHLP SGFLSEVSSLKHLDLSSNLLKTINKSALETKTTTKLSMLELHGNPFECTCDI  
GDFRRWMDEHLNVKIPRLVDVICASPGDQRGKSIVSLELTTCVSDVTAVILFFFTFFITT  
MVMLAALAHHLFYWDVWFIYNVCLAKVGYRSLSTSQTIFYDAYISYDTKDASVTDWVINE  
LRYHLEESRDKNVLLCLEERDWDPLAIIDNLMQSIQSKKTVFVLTKKYAKSWNFKTAF  
YLALQRLMDENMDVIIIFILLEPVLQHSQYLRLRQRICKSSILQWPDNPKAEGFLWQTLRN  
VVLTENDSRYNMYVDSIKQY

<1041 residues, 0 stop; molecular weight: 119856.26

**FIG. 3**

# REPLACEMENT SHEET

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CAAAATGACTCAGTTATTGACAGAGTCAGCAATCGTCGACTACAGGAAGTTCCCCAAACG
GTGGGCAAAATATGTGACAGAACTAGACCTGTCTGATAAATTTTCATCACACATAACGAAT
GAATCATTTCAAGGGCTGCAAAATCTCACATAAAATAAAATCTAAACCAACACCCCAATGTA
CAGCACCAAGAACGGAATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCA
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CCCTCTGGTTTGCCAGAGCTTTTGACAGAACTTAGTCTAATTCAAAACAATATATACAAC
ATACTAAAGAGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTTGGCCCTGGAAC
TGCTATTTAAACAAAAGTTTGCAGAGAAAATAACATAGAAGATGGAGTATTTGAAACGCTG
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GAACCTCAGAGAAGATGATTTCCAGCCCCCTGATGCAGCTTCCAAACTTATCGACTATCAAC
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```

FIG. 4A

# REPLACEMENT SHEET

GAAATTATTTACTTGTCTAGAAAAACAGAAATATCACCGTTGGTAAAAAGATACCCGGCAGAGT  
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GCTTATGGAAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCAAACCAA  
TTTGAAAAATCTTCCTGACATTCCTGTTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTG  
TTAAGTGGAACTGAATTTTCAGCCATTCTCATGTCAAAATATTTGGATTTGACAAACAAT  
AGACTAGACTTTTGATAATGCTAGTCTTTACTGAATTGTCCGACTTGGAAAGTTCTAGAT  
CTCAGCTATAATTACACTATTTTCAGAAATAGCAGCGGTAAACAATCATCTAGAATTTATT  
CAAAATTTCACAAATCTAAAAAGTTTAAACTTGAGCCACAACAACATTTATACCTTTAAACA  
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GACATTTGTGGAAATGATGATGACAAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAAT  
CTGACACGCTGTGGATTTATCCCTTAAATAGGTGAAGCACATCCCAAATGAAGCATTCCTT  
AATTTGCCAGCGAGTCTCACTGAACCTACATATAAATGATAAATATGTAAAGTTTTTTAAC  
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CATAACAGGATTTCCCACTTACCTCTGGCTTTCTTTCTGAAGTCAGTAGTCTGAAGCAC  
CTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAATCCGCACTTGAAACTAAGACC  
ACCACCAAATTATCTATGTTGGAACTACACGGAAACCCCTTTGAATGCACCTGTGACATTT  
GGAGATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTCACAGACTGGTAGAT  
GTCATTTGTGCCAGTCCCTGGGGATCAAGAGGGAAGAGTATTTGTGAGTCTGGAGCTAACA  
ACTTGTGTTTTCAGATGTCAGTGCAGTGATATTTATTTTCTTCACGTTCTTTATCACCACC  
ATGGTTATGTTGGCTGCCCTGGCTCACCATTGTTTTACTGGGATGTTTGGTTTATATAT  
AATGTGTGTTTAGCTAAGGTAAAGGCTACAGGTCTCTTTCCACATCCCAAACTTTCTAT  
GATGCTTACATTTCTTATGACACCAAAAGATGCCTCTGTTACTGACTGGGTGATAAATGAG

FIG. 4B

# REPLACEMENT SHEET

Sequence ss.DNA42663

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GAGCCAGTGTACAGCATCTCAGTATTGAGGCTACGGCAGCGGATCTGTAAGAGCTCC  
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GTGGTCTTGACTGAAAAATGATTACGGGTATAACAATATGTATGTCGATTCCAATTAAGCAA  
TACTAACTGACGTTAAGTCATGATTTCGCGCCATAATAAAGATGCAAGGAATGACATTT  
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CACATTTGCTGGCCACAGTTTTGAGGTCAGGAGTCCAGGCCCCAGCATAACTGGGTCC  
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GGGTCAACACTCATGTGGTGTGTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCAAAGG  
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CAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAAATCAAAAAAG  
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CTCCATGGGAGTGACCACTCAGTCCAGGGAAAAACAGCTGAAGACCAAGATGGTGAGCTC  
TGATTGCTTCAGTTGGTCACTCACTATTTTCCCTTGACTGCTGTCTGGGATGGCCTGCT  
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TGACCTAACACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCT  
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CTAAGGTTTAGATGCCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTC  
TTACCAATTTTTTAAAGTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGC  
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AAA

FIG. 4C

REPLACEMENT SHEET

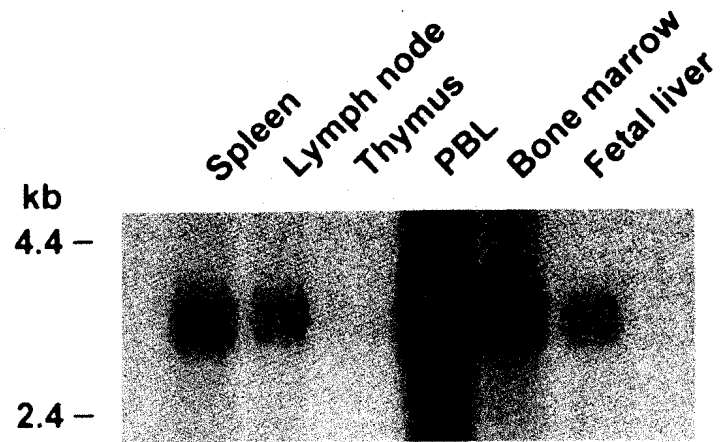


FIG. 5A

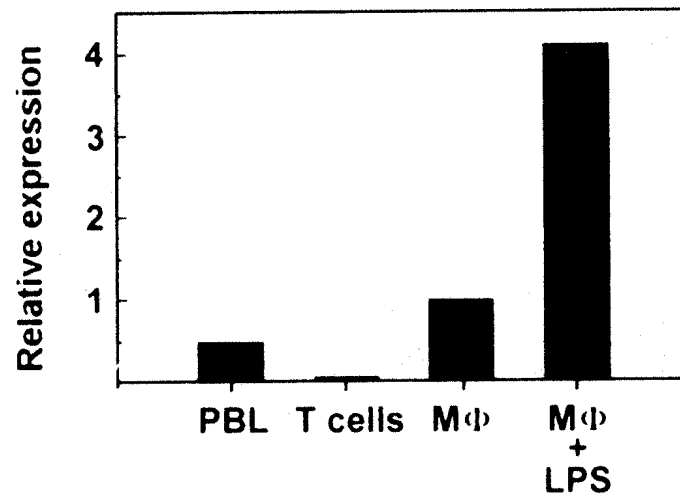


FIG. 5B



REPLACEMENT SHEET

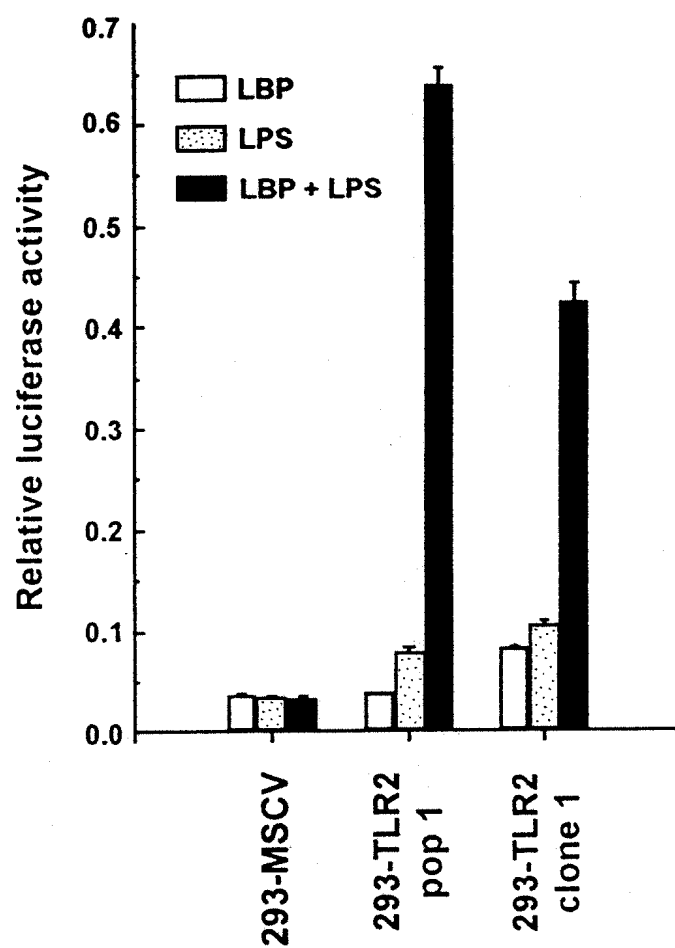


FIG. 6A

REPLACEMENT SHEET

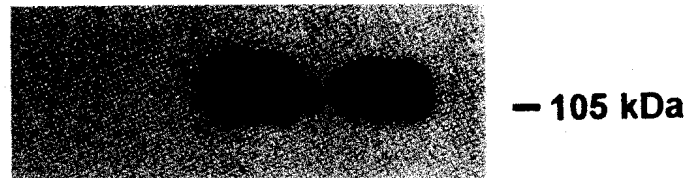


FIG. 6B

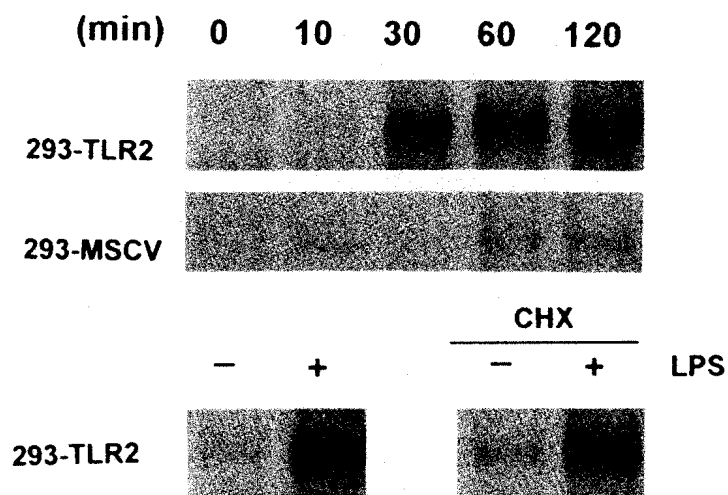


FIG. 6C

REPLACEMENT SHEET

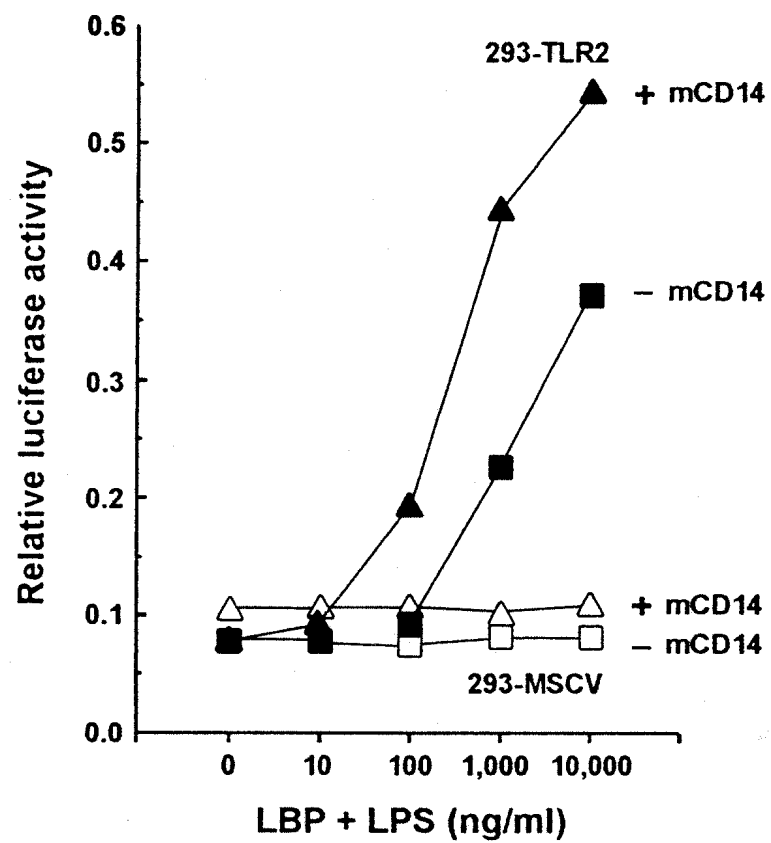


FIG. 6D

# REPLACEMENT SHEET

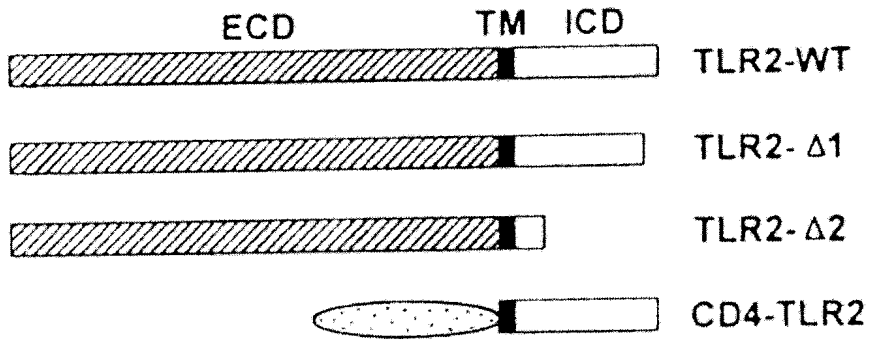


FIG. 7A

IL1-R	S A K T R F W K N V R Y H M P V	524
	:       :   :	
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	↑	
	TLR2-Δ1	

FIG. 7B

REPLACEMENT SHEET

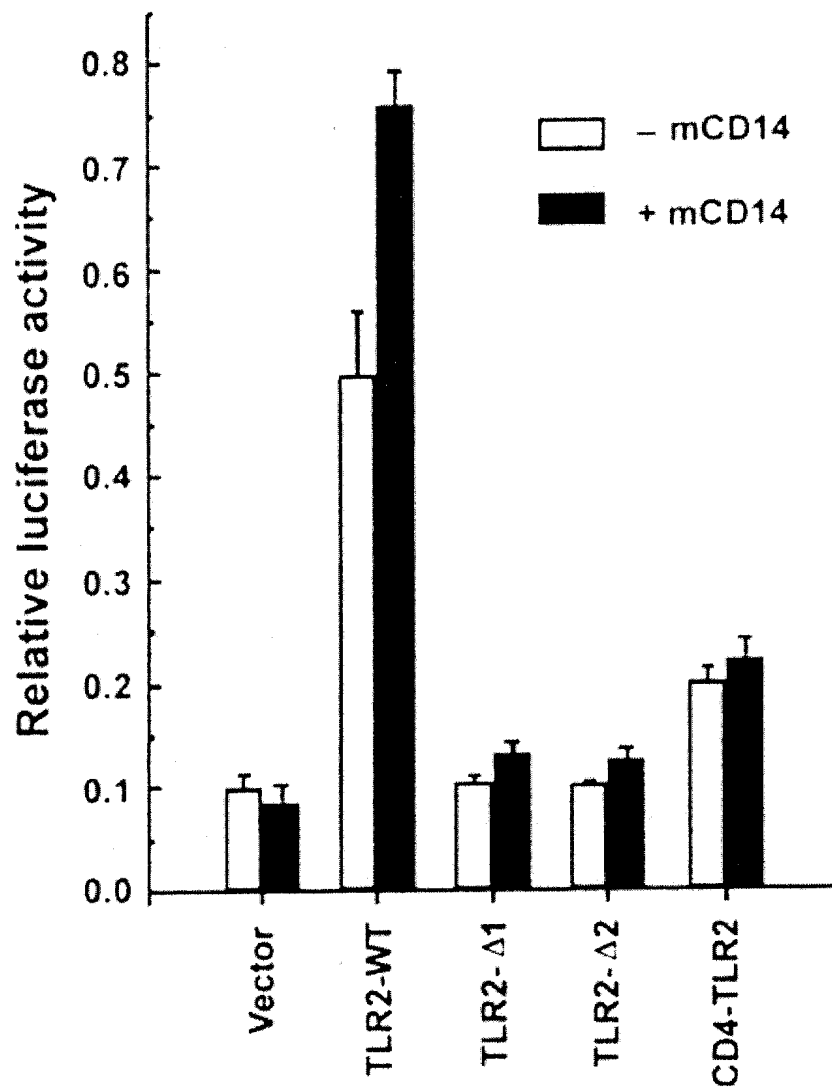


FIG. 7C

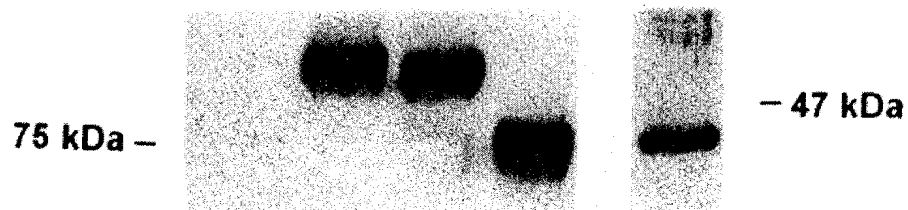


FIG. 7D

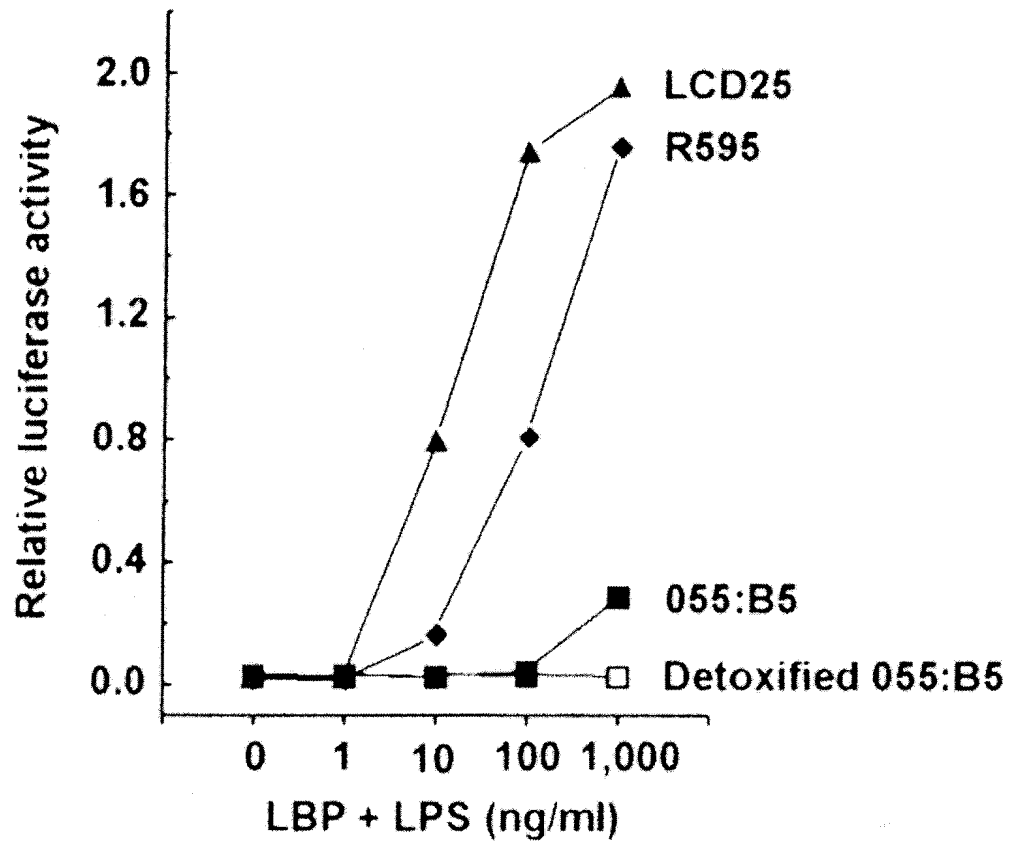


FIG. 8A

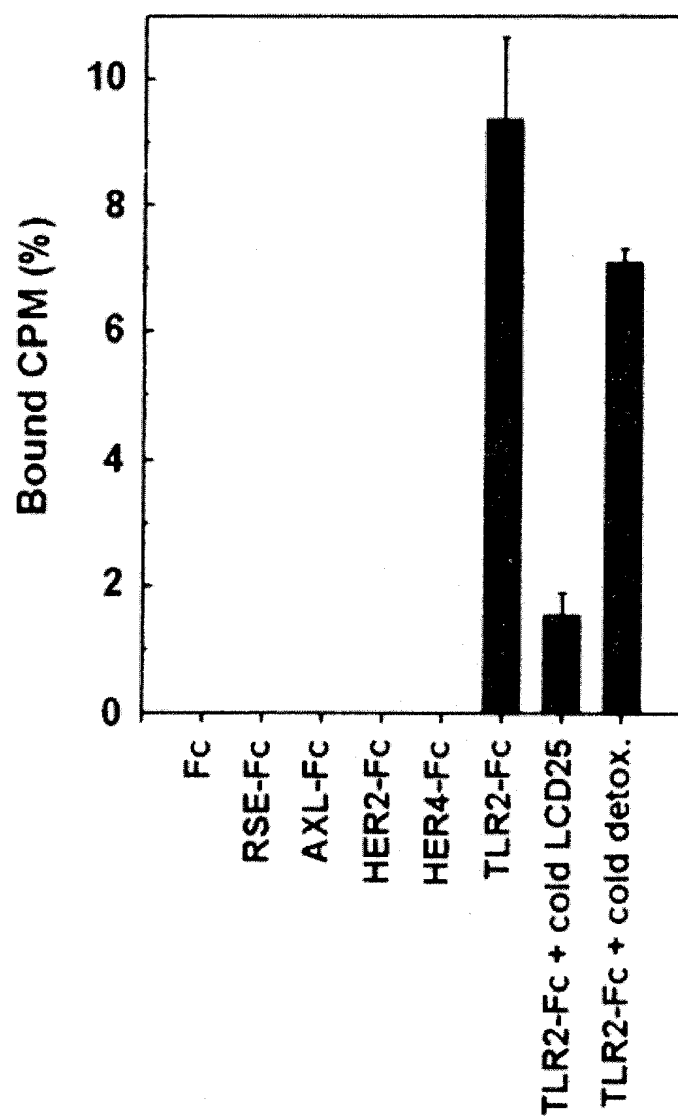


FIG. 8B

REPLACEMENT SHEET

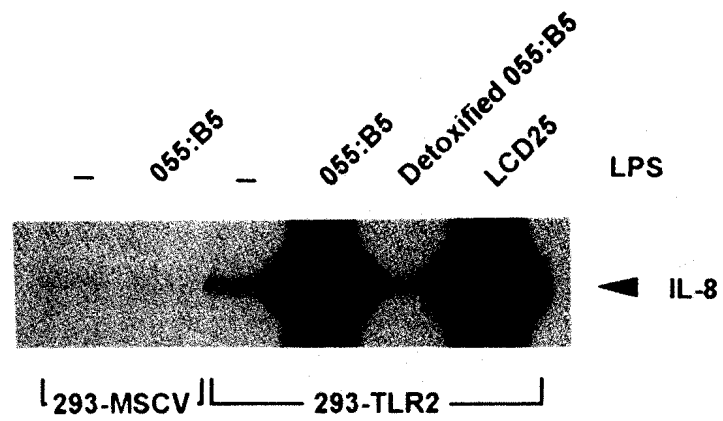


FIG. 9



## REPLACEMENT SHEET

GTTATGCCTAGAAAACATTTCTCAAGAATTAGAATTACGATATGCTGTCAAACACAATGA  
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FIG. 10

## REPLACEMENT SHEET

MPHTLWMVWVLGVIIISLSKEESSNQASLSCDRNGICKGSSGSLNSIPSGLTEAVKSLDL  
SNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSSLGSLEHLDLSYNYLSNLSSS  
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GNNFICSCEFLSFTQEQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLSVSECHRTAL  
VSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICYDAFVSYSE  
RDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTVFVLSNFV  
KSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKTYLEWPM  
EAQREGFWVNLRAAIKS

FIG. 11

# REPLACEMENT SHEET

(SEQ ID NO: 1)

Met Arg Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr Ala Glu Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu	30
1	5
Met Thr Asn Cys Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu	60
35	55
Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys His Asn Arg Ile Gln Leu Asp Leu Lys	90
65	85
Thr Phe Glu Phe Asn Lys Glu Leu Arg Tyr Leu Asp Tyr Leu Ser Asn Asn Arg Leu Lys Ser Val Thr Thr Tyr Leu Leu Ala Gly Leu Arg	120
95	115
Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp Thr Met Pro Ile Cys Glu Glu Ala Glu Asn Met Ser His Leu Glu Ile Leu Gly Leu Ser	150
125	145
Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln Lys Ile Ala His Leu His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro His Tyr	180
155	175
Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His Ile Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg Asp Gly	210
185	205
Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu	240
215	235
Asn Ala Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu Trp Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser	270
245	265

FIG. 12A

# REPLACEMENT SHEET

Val Glu His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala Tyr Leu Asp His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg	275	280	285	290	295	300
Thr Ile Lys Leu Glu His Val His Phe Arg Val Phe Tyr Ile Gln Gln Asp Lys Ile Tyr Leu Leu Thr Lys Met Asp Ile Glu Asn	305	310	315	320	325	330
Leu Thr Ile Ser Asn Ala Gln Met Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr Leu Asn Phe Ala Asn Asn Ile Leu	335	340	345	350	355	360
Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr Leu Ser Leu Val	365	370	375	380	385	390
Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser Trp Pro	395	400	405	410	415	420
Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu	425	430	435	440	445	450
Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp	455	460	465	470	475	480
Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser	485	490	495	500	505	510
Cys Gln Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys Glu Leu Lys Asn Phe Ile Gln Leu Thr Tyr Ser	515	520	525	530	535	540

FIG. 12B

# REPLACEMENT SHEET

Glu Val Met Met Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly Thr Arg Leu Lys Asp Val His Leu His	545	550	555	560	565	570
Glu Leu Ser Cys Asn Thr Ala Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala Val Ala Phe Cys Cys Leu His	575	580	585	590	595	600
Phe Asp Leu Pro Trp Tyr Trp Leu Arg Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln Glu Leu Lys Arg	605	610	615	620	625	630
Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp	635	640	645	650	655	660
Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser Tyr	665	670	675	680	685	690
Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu	695	700	705	710	715	720
Asn Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu	725	730	735	740	745	750
Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu	755	760	765	770	775	780
Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp Cys	785	790	795	800	805	810

Leu  
811

FIG. 12C

## REPLACEMENT SHEET

(SEQ ID NO: 2)  
GAATCATCCA CGCACTGCA GCTCTGCTGA GAGAGTGCAA GCCGTGGGG TTTTGAGCTC ATCTTCATCA TTCATATGAG GAATAAGTG GTAAAAATCCT 100  
<MET (trans=1-s, dir=f, res=1)>  
TGGAATACA ATGAGACTCA TCAGAAACAT TTACATATTT TGTAGATTG TTATGACAGC AGAGGTGAT GCTCCAGAGC TGCCAGAAAGA AAGGGAAGTG 200  
ATGACCAACT GCTCCAACAT GTCTCTAAGA AAGGTTCCCG CAGACTTGAC CCCAGCCACA ACGACACTGG ATTATCCTA TAACCTCCTT TTTCAACTCC 300  
AGAGTTCAGA TTTTCATTCT GTCTCCAAAC TGAGAGTTTTT GATTCTATGC CATAACAGAA TTCAACAGCT GGATCTCAA ACCTTGAAT TCAACAAGGA 400  
GTTAAGATAT TTAGATTGT CTAATAACAG ACTGAAGAGT GTAACCTGGT ATTTACTGGC AGGTCTCAGG TATTTAGATC TTTCTTTTAA TGACTTTGAC 500  
ACCATGCGCTA TCTGTGAGGA AGCTGGCAAC ATGTCACACC TGGAAATCCT AGGTTTGAGT GGGGCAAAAA TACAAAAATC AGATTTCAG AAAATTGCTC 600  
ATCTGCATCT AATACTGTC TTCTTAGGAT TCAGAACTCT TCCTCATTAT GAAGAAGTA GCCTGCCCAT CTTAAACACA ACAAACACTGC ACATTGTTTT 700  
ACCAATGGAC ACAAATTTCT GGGTTCTTTT GCGTGATGGA ATCAAGACTT CAAAAATATT AGAAATGACA AATATAGATG GCAAAAGCCA ATTTGTAAGT 800  
TATGAATGC AACGAAATCT TAGTTTAGAA AATGCTAAGA CATCGGTTCT ATTGCTTAAT AAAGTTGATT TACTCTGGGA CGACCTTTTC CTTATCTTAC 900  
AATTTGTTG GCATACATCA GTGGAACACT TTCAGATCCG AAATGTGACT TTTGGTGGTA AGGCTTATCT TGACCACAAAT TCATTTGACT ACTCAAATAC 1000  
TGTAATGAGA ACTATAAAAT TGGAGCATGT ACATTTTCAGA GTGTTTTACA TTCAACAGGA TAAATCTAT TTGCTTTTGA CCAAAATGGA CATAGAAAAC 1100  
CTGACAATAT CAAATGCACA AATGCCACAC ATGCTTTTCC CGAATTATCC TACGAAATTC CAATATTTAA ATTTTGCCAA TAATATCTTA ACAGACGAGT 1200  
TGTTTAAAAG AACTATCCAA CTGCCTCACT TGAAAACCTCT CATTTTGAAT GGCAATAAAC TGGAGACACT TTCTTTAGTA AGTTGCTTTG CTAACAACAC 1300  
ACCCTTGGAA CACTTGGATC TGAGTCAAAA TCTATTACAA CATAAAAAATG ATGAAAAATG CTCATGGCCA GAAACTGTGG TCAATATGAA TCTGTCATAC 1400  
AATAAATTGT CTGATTCTGT CTTCAGGTGC TTGCCCCAAA GTATTCAAAT ACTTGACCTA AATAATAACC AAATCCAAAC TGTACCTAAA GAGACTATTTC 1500  
ATCTGATGC CTTACGAGAA CTAATATATTG CATTTAATTT TCTAACTGAT CTCCTGGAT GCAGTCATTT CAGTAGACTT TCAGTTCTGA ACATTGAAAT 1600  
GAACCTTATT CTCAGCCCAT CTCTGGATTI TGTTCAGAGC TGCCAGGAAG TTAAAACTCT AAATGCGGGA AGAAATCCAT TCCGGTGTAC CTGTGAATTA 1700  
AAAAAATTTCA TTCAGCTTGA AACATATTCA GAGGTCTATGA TGGTTGGATG GTCAGATTCA TACACCTGTG AATACCCCTT AAACCTAAGG GGAACCTAGGT 1800

FIG. 13A

# REPLACEMENT SHEET

TAAAGACGT TCACTCCAC GAATTATCTT GCAACACAGC TCTGTTGATT GTCACCATTG TGGTTATTAT GCTAGTTCTG GGGTTGGCTG TGGCCTTCTG 1900  
 CTGCTCCAC TTGATCTGC CCTGGTATCT CAGGATGCTA GGTCAATGCA CACAAACATG GCACAGGCTT AGGAAACAA CCCAAGACA ACTCAAGAGA 2000  
 AATGTCGAT TCCACGCATT TATTTCATAC AGTGAACATG ATTCTCTGTG GGTGAGAAT GAATTGATCC CCAATCTAGA GAAGGAAGAT GGTCTATCT 2100  
 TGATTTGCCT TTATGAAAGC TACTTTGACC CTGGCAAAAG CATTAGTGAA AATATTGTAA GCTTCAITGA GAAAGCTAT AAGTCCATCT TTGTTTTGTC 2200  
 TCCCAACTTT GTCCAGAAATG AGTGGTGCCA TTATGAATTC TACTTTGCC ACCACAATCT CTTCATGAA AATTCTGATC ATATAATTCT TATCTTACTG 2300  
 GAACCAATC CATTCTATTG CATTCCACC AGGTATCATA AACTGAAAGC TCTCTGGAA AAAAAAGCAT ACTTGAATG GCCCAAGGAT AGGCGTAAAT 2400  
 GTGGGCTTTT CTGGGCAAC CTTCGAGCTG CTATTAATGT TAATGTATTA GCCACCAGAG AATGTATGA ACTGCAGACA TTCACAGAGT TAAATGAAGA 2500  
 GTCTCGAGGT TCTACAATCT CTCTGATGAG AACAGATTGT CTA TAA AATC CCACAGTCTT TGGGAAGTTG GGGACCACAT ACACTGTTGG GATGTACATT 2600  
 GATACAACTT TTATGATGGC AATTGACAA TATTTATTAA AATAAAAAAT GGTATTCTCC TTCTATATCAG TTTCTAGAAG GATTTCTAAG AATGTATCCT 2700  
 ATAGAAACAC CTTTCAAGT TTATAAGGC TTATGAGGC AGGTGTTCTAT CCCAGGATTG TTTATAATCA TGAAAAATGT GGCACAGTGC AGTGGCTCAC 2800  
 TCTTGTAATC CCAGCACTAT GGGAGGCCAA GGTGGGTGAC CCACGAGGTC AAGAGATGGA GACCATCTCTG GCCAACATGG TGAACCCCTG TCTCTACTAA 2900  
 AAATACAAA ATTAGCTGG CGTGATGGTG CACGCTGTA GTCCAGCTA CTGGGAGGC TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGCAGTTG 3000  
 CAGTGAGCTG AGATCGAGCC ACTGCCTCC AGCCTGGTGA CAGAGCGAGA CTCCATCTCA AAAAAAGAA AAAAAAAA GAAAAAATG GAAAAATCC 3100  
 TCATGGCCAC AAAATAAGGT CTAATTCAAT AAATTATAGT ACATTAATGT AATATAATAT TACATGCCAC TAAAAAGAT AAGGTAGCTG TATATTTCTT 3200  
 GGTATGGAA AACATATTA ATATGTTATA AACTATTAGG TTGGTGCAA ACTAATTGT GTTTTTGCCA TTGAAATGGC ATTGAATAA AAGTGTAAAG 3300  
 AATCTATAC CAGATGTAGT AACAGTGGT TGGGTCTGG AGGTTGGATT ACAGGGAGCA TTTGATTTCT ATGTTGTGTA TTTCTATAAT GTTTGAATTG 3400  
 TTTAGAATGA ATCTGTATTT CTTTATAAG TAGAAAAA AATAAGATAG TTTTACAGC CT 3462

FIG. 13B